

01/24

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/732,597
DATE: 12/21/2000
TIME: 10:15:55

Input Set : A:\BB1413 US NA Seq Listing.txt
Output Set: N:\CRF3\12212000\I732597.raw

ENTERED

```

2 <110> APPLICANT: Cahoon, Edgar B.
3   Cahoon, Rebecca E.
5 <120> TITLE OF INVENTION: Enzymes Involved In Petroselinic Acid Biosynthesis
7 <130> FILE REFERENCE: BB1413 US NA
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/732,597
C--> 10 <141> CURRENT FILING DATE: 2000-12-08
12 <150> PRIOR APPLICATION NUMBER: 60/169,968
W--> 13 <151> PRIOR FILING DATE: 9 DECEMBER 1999
15 <160> NUMBER OF SEQ ID NOS: 12
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1344
21 <212> TYPE: DNA
22 <213> ORGANISM: Hedera helix
24 <220> FEATURE:
25 <221> NAME/KEY: unsure
26 <222> LOCATION: (997)
28 <400> SEQUENCE: 1
29 caaccccaga aaataaaaaat aaaaactcaa gaagaagaag aaqaaatggc tttgaagctc 60
30 aatttccaat gcaagaagaa ccacccctgct gcgttttcta agtcaccatt accagtgacc 120
31 agagttagct ctccaagggt ttctcatggt tccactgtca actctaactc catggttctt 180
32 gataaattca aaagtccgcc aaatcttcaa gtcaactcaact ctatgccacc ccaaaagcta 240
33 gaaatattca agtcccttga tgattgggct aggaacaatg tgttgattca cctcaaatct 300
34 gtcgagaaat cttaggcaacc acaagactac ttgccggatc cgggtgcaga cggattcgag 360
35 gagcaagtgc gggagtttag ggaaggggcc aaggagattc ccgacgacta ttttgtggtg 420
36 ttagttggag atatgatcac agaagaagca ctccaacat atatgtctat gtcgaatagg 480
37 tgtgatggtt ttaaggatga gactggggct gagcccgatg cttgggcaat gtggactagg 540
38 gcatggactg ccgaagagaa tagacatggt gaccttctca ataagtacct ttatttgtct 600
39 ggaagggttg atatgaggaa aattgagaag actattcaat atctcatcgg ctcaaggaaatg 660
40 gatattcaagt cagaaaaacag cccctaccta ggcttcatct acacatcctt ccaagagaga 720
41 gcaaccttca tatcccatgc caacacagcc aagctggccc aacactacgg cgaagaagac 780
42 ctgcgtcaca tctgcggctc catcgcttcc gacgagaagc gccacgdcac agcctacacc 840
43 aagatcgttg aaaagctcgc tgagatcgac ccgacacaaa cagtaattgc ttttgcagat 900
44 atgatgcgca aaaaaataac aatgccagcg cacttgatgt acgacggaag tgacgaactt 960
W--> 45 ctttttaaac atttcacggc ggttgctcag agagtgnngg tttattctgc gttggattat 1020
46 tgcgacatct tagagtttct ggtggataaa tgggaatgtg aaaggcttac ggggctgtcg 1080
47 gacgaggggc gaaagcgca ggaatatgtg tgtgaattgg gtcccaagat taggcgagtg 1140
48 gaagagaaag tgcaggggaa ggagaagaag aagaaagctg agcaccctgt ttctttcagc 1200
49 tggattttca atcgggagtt gaagatatga acaggaaggg aagggaatgg aggagcaaat 1260
50 gagtgtagta gatttctata tgcatyttta tatattatga atgattatta tataataata 1320
51 agtgtttgag ttttaagtta aaaa 1344
53 <210> SEQ ID NO: 2
54 <211> LENGTH: 394
55 <212> TYPE: PRT
56 <213> ORGANISM: Hedera helix
58 <220> FEATURE:
59 <221> NAME/KEY: UNSURE

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60 <222> LOCATION: (318)
62 <400> SEQUENCE: 2
63 Met ala Leu Lys Leu Asn Phe Gln Cys Lys Lys Asn His Pro Ala Ala
64 1 5 10 15
66 Phe Ala Lys Ser Pro Leu Pro Val Thr Arg Val Ser Ser Pro Arg Val
67 20 25 30
69 Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
70 35 40 45
72 Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
73 50 55 60
75 Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
76 65 70 75 80
78 Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
79 85 90 95
81 Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Val Arg Glu Leu Arg
82 100 105 110
84 Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
85 115 120 125
87 Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
88 130 135 140
90 Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
91 145 150 155 160
93 Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
94 165 170 175
96 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
97 180 185 190
99 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
100 195 200 205
102 Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
103 210 215 220
105 Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
106 225 230 235 240
108 Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
109 245 250 255
111 Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
112 260 265 270
114 Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
115 275 280 285
117 Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
118 290 295 300
W--> 120 Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr
121 305 310 315 320
123 Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
124 325 330 335
126 Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
127 340 345 350
129 Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
130 355 360 365
132 Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe

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133      370      375      380
135 Ser-Trp Ile Phe Asn Arg Glu Leu Lys Ile
136 385      390
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 445
140 <212> TYPE: DNA
141 <213> ORGANISM: Hedera helix
143 <400> SEQUENCE: 3
144 ctctgtgtc tccgctctt gttttttct ctttccaaat attttctgag taattttctc 60
145 agatctattc ctctttcttc tctccctaatt ttgatccatc aatggcttct gttactgcct 120
146 catcgatttc cttcactctc atcgcaagct cctcgaagca aaaccaggga cttgccaaaga 180
147 gttcaatttc actctctgtc aatgggaaat ccttcggttc acttaggttg ctgtcggcac 240
148 cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
149 ttgtgcggaa acaactggcg ctgcgctga ttctgcaagt cactggagag tcaaaattcg 360
150 cagcgttgg ggtgattct ctgcacacgg ttgagattgt gatgggacta aaggaggaaat 420
151 tcggaatcaa gctgggaaa aagaa 445
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 114
155 <212> TYPE: PRT
156 <213> ORGANISM: Hedera helix
158 <400> SEQUENCE: 4
159 Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser
160 1 5 10 15
162 Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser
163 20 25 30
165 Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
166 35 40 45
168 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
169 50 55 60
171 Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val
172 65 70 75 80
174 Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
175 85 90 95
177 Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly
178 100 105 110
180 Lys Lys
181 114
183 <210> SEQ ID NO: 5
184 <211> LENGTH: 920
185 <212> TYPE: DNA
186 <213> ORGANISM: Hedera helix
188 <400> SEQUENCE: 5
189 ctctgtgtc tccgctctt gttttttct ctttccaaat attttctgag taattttctc 60
190 agatctattc ctctttcttc tctccctaatt ttgatccatc aatggcttct gttactgcct 120
191 catcgatttc cttcactctc atcgcaagct cctcgaagca aaaccaggga cttgccaaaga 180
192 gttcaatttc actctctgtc aatgggaaat ccttcggttc acttaggttg ctgtcggcac 240
193 cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300
194 ttgtgcggaa acaactggcg ctgcgctga ttctgcaagt cactggagag tcaaaattcg 360
195 cagcgttgg ggtgattct ctgcacacgg ttgagattgt gatgggacta gaggaggaaat 420

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```

196 tcggaatcag cgtggaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480
197 acctgattga gaagcttgtt gaaaaaaagg agtagaagaa cgggggtaga aattctgcaa 540
198 aatagggtta ttaaggacag ttactttatt aggatgttc atcaagatct tcattaccct 600
199 acatttattt gtatgtctct catgaagccg caaaagtatg agtgggtgatg aaattttacc 660
200 cgagttcttc ccttaattat caaagtgaga gagccagaaa aagaggctat gctatctctc 720
201 atctcgatat gttttatttt cttgtcggac ttctgggttg agtttttttt ttttatctaa 780
202 acatgatatt agtcttgttt aaaagtctct caaaaaata tatcttgttg ttgagactga 840
203 tggagttatt gctcttgata ttttgaatgt attttgagtt attcaaaaaa aaaaaaaaaa 900
204 aaaaaaaaaa aaaaaaaaaa 920

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207 <210> SEQ ID NO: 6

208 <211> LENGTH: 137

209 <212> TYPE: PRT

210 <213> ORGANISM: Hedera helix

212 <400> SEQUENCE: 6

213 Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser

214 1 5 10 15

216 Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser

217 20 25 30

219 Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu

220 35 40 45

222 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val

223 50 55 60

225 Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val

226 65 70 75 80

228 Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr

229 85 90 95

231 Val Glu Ile Val Met Gly Leu Glu Glu Phe Gly Ile Ser Val Glu

232 100 105 110

234 Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu

235 115 120 125

237 Ile Glu Lys Leu Val Glu Lys Lys Glu

238 130 135

241 <210> SEQ ID NO: 7

242 <211> LENGTH: 385

243 <212> TYPE: PRT

244 <213> ORGANISM: Coriandrum sativum

246 <400> SEQUENCE: 7

247 Met Ala Met Lys Leu Asn Ala Leu Met Thr Leu Gln Cys Pro Lys Arg

248 1 5 10 15

250 Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser

251 20 25 30

253 Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp

254 35 40 45

256 Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu

257 50 55 60

259 Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu

260 65 70 75 80

262 Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala

263 85 90 95

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TIME: 10:15:56

Input Set : A:\BB1413 US NA Seq Listing.txt

Output Set: N:\CRF3\12212000\I732597.raw

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265 Phe Glu Asp Glu Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro
266           100           105           110
268 Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala
269           115           120           125
271 Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp
272           130           135           140
274 Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp
275 145           150           155           160
277 Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr
278           165           170           175
280 Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr
281           180           185           190
283 Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met
284           195           200           205
286 Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
287           210           215           220
289 Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala
290 225           230           235           240
292 Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala
293           245           250           255
295 Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr
296           260           265           270
298 Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala
299           275           280           285
301 His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr
302           290           295           300
304 Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp
305 305           310           315           320
307 Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly
308           325           330           335
310 Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala
311           340           345           350
313 Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys
314           355           360           365
316 Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile
317           370           375           380
319 Ile
320 385
322 <210> SEQ ID NO: 8
323 <211> LENGTH: 137
324 <212> TYPE: PRT
325 <213> ORGANISM: Coriandrum sativum
327 <400> SEQUENCE: 8
328 Met Ala Ala Phe Thr Ala Ser Ser Val Ser Phe Thr Pro Leu Ser Ile
329 1           5           10           15
331 Ser Leu Asn Gln Thr Lys Gly Phe Ala Arg Gly Ser Val Ser Ile Pro
332           20           25           30
334 Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu
335           35           40           45

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/732,597

DATE: 12/21/2000

TIME: 10:15:57

Input Set : A:\BB1413 US NA Seq Listing.txt

Output Set: N:\CRF3\12212000\I732597.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:45 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:45 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:120 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:120 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2